

165										170					175				
Ala	Asp	Val	Ala	Arg	Gly	Gly	Asp	Leu	Phe	Arg	Leu	Asn	Cys	Ala	Ser				
			180						185				190						
Cys	His	Asn	Phe	Thr	Gly	Arg	Gly	Gly	Ala	Leu	Ser	Ser	Gly	Lys	Tyr				
		195					200					205							
Ala	Pro	Asn	Leu	Asp	Ala	Ala	Asn	Glu	Gln	Glu	Ile	Tyr	Gln	Ala	Met				
	210					215					220								
Leu	Thr	Gly	Pro	Gln	Asn	Met	Pro	Lys	Phe	Ser	Asp	Arg	Gln	Leu	Ser				
225					230					235					240				
Ala	Asp	Glu	Lys	Lys	Asp	Ile	Ile	Ala	Phe	Ile	Lys	Ser	Thr	Lys	Glu				
				245					250						255				
Thr	Pro	Ser	Pro	Gly	Gly	Tyr	Ser	Leu	Gly	Ser	Leu	Gly	Pro	Val	Ala				
			260					265						270					
Glu	Gly	Leu	Phe	Met	Trp	Val	Phe	Gly	Ile	Leu	Val	Leu	Val	Ala	Ala				
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Ala	Met	Trp	Ile	Gly	Ser	Arg	Ser												
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 <223> RXN03096

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 Met Val Leu Val Trp 5
 1

tcc aag gcc ttc tgg cgc gac cgt aaa gac gcc ccc gat gga gca acc 163
 Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp Ala Pro Asp Gly Ala Thr 20
 10 15

gca cta gca aga ccc gca cct ttg gta gat atc caa gac gaa gtc gcc 211
 Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Ile Gln Asp Glu Val Ala 35
 25 30

gtt aaa gac cgc aac gat gtc gga cgg atg cct tgg ggc atg gtc ttc 259
 Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro Trp Gly Met Val Phe 50
 40 45

tcc act gcc ctg ttg gtt tcc gca tcc ctt gct gta tcc gtg ctc gca 307
 Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala Val Ser Val Leu Ala 65
 55 60

gga cca ctg tca tct att act gga cgc gcc gcc gaa tcc gca caa gat 355

Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala Glu Ser Ala Gln Asp
 70 75 80 85
 gtc aac atc tac cgc gcc gca gta ctc ggc cca act acc tcg acc cat 403
 Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro Thr Thr Ser Thr His
 90 95 100
 cac gca cac tcg aga tgg agc gtt acg acg cca acc gcg atg aca tca 451
 His Ala His Ser Arg Trp Ser Val Thr Thr Pro Thr Ala Met Thr Ser
 105 110 115
 acc acc gcg tcg aca cca atg gaa cgg agg acc aac cat gat cag tgg 499
 Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr Asn His Asp Gln Trp
 120 125 130
 att 502
 Ile

<210> 746
 <211> 134
 <212> PRT
 <213> Corynebacterium glutamicum

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 Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Ile
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 Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro
 35 40 45
 Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala
 50 55 60
 Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala
 65 70 75 80
 Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro
 85 90 95
 Thr Thr Ser Thr His His Ala His Ser Arg Trp Ser Val Thr Thr Pro
 100 105 110
 Thr Ala Met Thr Ser Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr
 115 120 125
 Asn His Asp Gln Trp Ile
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<210> 747
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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<223> RXN02036

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gccctcatct ctgctgcagt ggcggctctc ggagggtggt gtg cat att cct ttt 115
 Val His Ile Pro Phe
 1 5

ggg cac ctc gcc gac acc gtc tcc tgg gac tgc ggg gga ggc agc tgc 163
 Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys Gly Gly Gly Ser Cys
 10 15 20

gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt 211
 Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser
 25 30 35

acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct 259
 Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala
 40 45 50

ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc ggc gtg 307
 Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val
 55 60 65

cag gct gcg att gcc gac ggc tac acg tcc gcg act tcc gtc ggc ttc 355
 Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe
 70 75 80 85

gaa atg act gtc tgc ctc att ctt ttc atc atc gca ggt ctg tgc ttt 403
 Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe
 90 95 100

ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag 451
 Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys
 105 110 115

gtc cgc gag agg gct gcg ggc ttg agc aat taggctctcg cttttcgacg 501
 Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
 120 125

ttt 504

<210> 748

<211> 127

<212> PRT

<213> Corynebacterium glutamicum

<400> 748

Val His Ile Pro Phe Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys
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Gly Gly Gly Ser Cys Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro
 20 25 30

Ala Ala Phe Met Ser Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala
 35 40 45

Ile Gly Leu Ile Ala Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala

50 55 60

Phe Arg Ser Gly Val Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala
65 70 75 80

Thr Ser Val Gly Phe Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile
 85 90 95

Ala Gly Leu Cys Phe Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg
 100 105 110

Gln Val Ala Arg Lys Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
 115 120 125

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<211> 882
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(859)
<223> RXN02765

<400> 749

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ttcaaccttat ggccgtatat tcgcggattt taggagataa atg tctaat caatta 115
MetSerAsnGlnLeu
15

cgcgatcacgtcgcgacgccttccaagtggcgaggacctgccgaa 163
ProAspHisValArgAspAlaPheGlnValGlyAlaGlyProAlaGlu
101520

caa ctcggtcaa gcttggttcggatctcgctggc aaactgtg 211
GlnLeuGlyGlnAlaTrpAspPheGlyPheArgValGlyAsnThrVal
253035

ttc gccaaa gtgacggcgcg gaa gtgtcgggc ttgtcg tcg aaa acc 259
PheAlaLysValThrAlaProGluValSerGlyTrpSerSerLysThr
404550

cgc gaaccctgaaaa ccagaagggcgtgcgcgtcgtacgacgc 307
ArgGluThrLeuLysProGluGlyValArgValValArgProIleArg
556065

tcc accgacggc cgatttgtgtgcgggtggc gcacgtgtgttc 355
SerThrAspGlyArgPheValValAlaGlyTrpArgAlaSerValPhe
70758085

tct acgggaacg atc agcaagcga gtc gat gag acg gtc gtt gcg ggt 403
SerThrGlyThrIleSerLysArgValAspGluThrValValAlaGly
9095100

ctt cgtttg gcatgat gca tta gtggat acg cat gca ccg gaa cct gtg 451
LeuArgLeuAlaAspAlaLeuValAspThrHisAlaProGluProVal
105110115

gac aatgtgtttaac cgtgctgatgtgcag gcc tgg gaa gag cagccc 499

Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala Trp Glu Glu Gln Pro
 120 125 130
 ggt cga atc ggt gaa ttg ttg gag ccg att aat cgc gtg aac cag gtt 547
 Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn Arg Val Asn Gln Val
 135 140 145
 ggt cat gcg gat atg ttg gcg aca acg ctg tat gcg gga act cag cca 595
 Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr Ala Gly Thr Gln Pro
 150 155 160 165
 cct gca gtg acg gat ttg gtg cca gtg ctg cgt ccg cat ggt ttc act 643
 Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg Pro His Gly Phe Thr
 170 175 180
 gcg gca ttg gtg atc gtt gat ggg ttg ctg ctg ggt gcg gtt gat gag 691
 Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu Gly Ala Val Asp Glu
 185 190 195
 gga att ctg cgg agg ttt tcg cat ttg ccg gaa att gag cag ctg gtt 739
 Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu Ile Glu Gln Leu Val
 200 205 210
 ttg agg gca ttt ttg ttc cgt cga aac ttg cag gag ttc tct gag aac 787
 Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln Glu Phe Ser Glu Asn
 215 220 225
 aac gat ccg aat gtt att tcg aac cta aac agg gtg gaa tcg aca ctc 835
 Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg Val Glu Ser Thr Leu
 230 235 240 245
 gtg tcg tat gtt tct gac aag att tgaggtatgt cggaatacaa acc 882
 Val Ser Tyr Val Ser Asp Lys Ile
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<210> 750

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 750

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 20 25 30
 Val Gly Asn Thr Val Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly
 35 40 45
 Trp Ser Ser Lys Thr Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val
 50 55 60
 Val Arg Pro Ile Arg Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp
 65 70 75 80
 Arg Ala Ser Val Phe Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu
 85 90 95
 Thr Val Val Ala Gly Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His

<400> 751																		
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accttatgac	ctcagtagtg	tggtgggcgt	gaaacagcga		atg	gtc	ggt	tca	agt								115	
					Met	Val	Gly	Ser	Ser									
						1				5								
ggt ttg	cgg gta	tcc agg	ctc ggt	ttg ggc	acc tca	aca tgg	ggc tcg										163	
Gly Leu	Arg Val	Ser Arg	Leu Gly	Leu Gly	Thr Ser	Thr Trp	Gly Ser											
		10		15			20											
ggc acc	gag ctg	gct gag	gca ggc	gat atc	ttt aag	gcg ttc	atc aat										211	
Gly Thr	Glu Leu	Ala Glu	Ala Gly	Asp Ile	Phe Lys	Ala Phe	Ile Asn											
		25		30		35												
tct ggt	ggc acg	ctt atc	gac gtc	tcc ccc	aac tac	acc acc	ggc gtc										259	
Ser Gly	Gly Thr	Leu Ile	Asp Val	Ser Pro	Asn Tyr	Thr Thr	Gly Val											
	40		45			50												
gcg gaa	gaa atg	ctc ggc	acg atg	ttg gat	gcg gaa	gtc tct	cgt tcg										307	
Ala Glu	Glu Met	Leu Gly	Thr Met	Leu Asp	Ala Glu	Val Ser	Arg Ser											

55	60	65	
gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc	355		
Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu			
70 75 80 85			
ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat	403		
Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp			
90 95 100			
gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg	451		
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val			
105 110 115			
ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg	499		
Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu			
120 125 130			
gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga	547		
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly			
135 140 145			
tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca	595		
Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala			
150 155 160 165			
gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg	643		
Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu			
170 175 180			
ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta	691		
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu			
185 190 195			
ggg gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act	739		
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr			
200 205 210			
gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca	787		
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr			
215 220 225			
gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc	835		
Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile			
230 235 240 245			
att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc	883		
Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro			
250 255 260			
gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct	931		
Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala			
265 270 275			
gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag	979		
Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys			
280 285 290			
gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat	1027		
Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp			
295 300 305			

gtc tcc ctg tgacttggtc caattacatt cac
 Val Ser Leu
 310

1059

<210> 752
 <211> 312
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 752
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 Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe
 20 25 30
 Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn
 35 40 45
 Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala
 50 55 60
 Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn
 65 70 75 80
 Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu
 85 90 95
 Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu
 100 105 110
 Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu
 115 120 125
 Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr
 130 135 140
 Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
 145 150 155 160
 Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
 165 170 175
 Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
 180 185 190
 Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
 195 200 205
 Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
 210 215 220
 Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
 225 230 235 240
 Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
 245 250 255
 Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg


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                260                265                270
Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
   275                280                285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
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Gln Ala Leu Asp Asp Val Ser Leu
305                310

<210> 753
<211> 747
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(724)
<223> RXN02554

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                               Met Ser His Thr Lys
                               1                5

cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc 163
Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala
           10                15                20

agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt 211
Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly
           25                30                35

gct gtg gac aaa atc gct ctt acc gct gag atc ctt atg ccc ggc gcg 259
Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala
           40                45                50

gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc 307
Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe
           55                60                65

ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta 355
Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu
           70                75                80                85

gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat 403
Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn
           90                95                100

ggt gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att 451
Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile
           105                110                115

att gcg gag ttt ttc gcg gga tca acc atg gtg aag tct ttt aac cac 499
Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val Lys Ser Phe Asn His
           120                125                130

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Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile
    135                140                145

gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta 595
Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu
    150                155                160                165

att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac 643
Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn
                170                175                180

ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat 691
Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn
                185                190                195

aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744
Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
    200                205

aac 747

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<210> 754
 <211> 208
 <212> PRT
 <213> Corynebacterium glutamicum

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          20          25          30

Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile
          35          40          45

Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp
  50          55          60

Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val
  65          70          75          80

Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His
          85          90          95

Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg
          100          105          110

Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val
          115          120          125

Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly
          130          135          140

Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala
          145          150          155          160

Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile
          165          170          175

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Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe
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Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
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<210> 755

<211> 933

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(910)

<223> RXN01204

<400> 755

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ccgaacacgg gagagaacgc tgagcggttac aacactgtcc atg aag ggc gaa ttc 115
 Met Lys Gly Glu Phe
 1 5

cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat 163
 His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp
 10 15 20

agt ggt gaa gtc gtg aac atg ctg ttc acc gat ttc gct aat ggt tgg 211
 Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp
 25 30 35

ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc 259
 Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu Leu Met Thr Ala Val
 40 45 50

gtt gtg gtc ttc ttc ctt tgg gct atg cgc aag cca aag ctt gtt ccg 307
 Val Val Val Phe Phe Leu Trp Ala Met Arg Lys Pro Lys Leu Val Pro
 55 60 65

cat ggc gtc cag aat ttt gca gag tac gca ctc gat ttc gtt ggt att 355
 His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu Asp Phe Val Gly Ile
 70 75 80 85

cac atc gct gaa gac atc ctc gga aag aag aaa ggt cgt cgg ttc ctg 403
 His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys Gly Arg Arg Phe Leu
 90 95 100

ccg atc ctg gcc acc atc ttc ttc gcg gct ctg ttg atg aac ctt gca 451
 Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu Leu Met Asn Leu Ala
 105 110 115

acg atc atc ccg gga cta aac atc tcc tcc aac tca cgt att gca ttc 499
 Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn Ser Arg Ile Ala Phe
 120 125 130

cca atc gtg atg gcg gta gct ggt tac atc gcg ttt atc tac gca ggc 547

Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala Phe Ile Tyr Ala Gly
 135 140 145

tct aag cgt tac gga ttc ttc aaa tat gtg aag tct tct gtt gtg att 595
 Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys Ser Ser Val Val Ile
 150 155 160 165

ccg aac att cca cca gca ctt cac gtc ttg gtg gtt cca att gag ttc 643
 Pro Asn Ile Pro Pro Ala Leu His Val Leu Val Val Pro Ile Glu Phe
 170 175 180

ttc tct aca ttc atc ttg agg cca gtc acc ctg gca ctg cgt ttg atg 691
 Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu Ala Leu Arg Leu Met
 185 190 195

gcc aac ttc ctt gct ggc cac atc atc ctg gtt ctg ctt ttc tcc gca 739
 Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val Leu Leu Phe Ser Ala
 200 205 210

acg aac ttc ttc ttc ttc cag ttc aac gga tgg aca gca atg tcc ggc 787
 Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp Thr Ala Met Ser Gly
 215 220 225

gta acc atc ttg atg gca gta ctc ttc acg gtt tac gag atc att gtt 835
 Val Thr Ile Leu Met Ala Val Leu Phe Thr Val Tyr Glu Ile Ile Val
 230 235 240 245

atc ttc ctg cag gca tac atc ttc gct ctg ctg gtc gct gta tac att 883
 Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu Val Ala Val Tyr Ile
 250 255 260

gag ctt tca ctt cac gcg gat tct cac tagatgaaaa aggtcgcctat 930
 Glu Leu Ser Leu His Ala Asp Ser His
 265 270

taa 933

<210> 756

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 756

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Gly His Val Thr Asp Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp
 20 25 30

Phe Ala Asn Gly Trp Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu
 35 40 45

Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys
 50 55 60

Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu
 65 70 75 80

Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys
 85 90 95

Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu
 100 105 110
 Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn
 115 120 125
 Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala
 130 135 140
 Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys
 145 150 155 160
 Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val
 165 170 175
 Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu
 180 185 190
 Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val
 195 200 205
 Leu Leu Phe Ser Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp
 210 215 220
 Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val
 225 230 235 240
 Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu
 245 250 255
 Val Ala Val Tyr Ile Glu Leu Ser Leu His Ala Asp Ser His
 260 265 270

<210> 757
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(862)
 <223> FRXA01204

<400> 757
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 Met Lys Gly Glu Phe
 1 5
 cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat 163
 His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp
 10 15 20
 agt ggt gaa gtc gtg aac atg ctg ttc acc gat ttc gct aat ggt tgg 211
 Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp
 25 30 35
 ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc 259

Phe	Ala	Met	Asp	Arg	Ile	Val	Leu	Ile	Arg	Leu	Leu	Met	Thr	Ala	Val		
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ggt	gtg	gtc	ttc	ttc	ctt	tgg	gct	atg	cgc	aag	cca	aag	ctt	ggt	ccg	307	
Val	Val	Val	Phe	Phe	Leu	Trp	Ala	Met	Arg	Lys	Pro	Lys	Leu	Val	Pro		
		55				60					65						
cat	ggc	gtc	cag	aat	ttt	gca	gag	tac	gca	ctc	gat	ttc	ggt	ggg	att	355	
His	Gly	Val	Gln	Asn	Phe	Ala	Glu	Tyr	Ala	Leu	Asp	Phe	Val	Gly	Ile		
		70			75					80					85		
cac	atc	gct	gaa	gac	atc	ctc	gga	aag	aag	aaa	ggt	cgt	cgg	ttc	ctg	403	
His	Ile	Ala	Glu	Asp	Ile	Leu	Gly	Lys	Lys	Lys	Gly	Arg	Arg	Phe	Leu		
				90					95					100			
ccg	atc	ctg	gcc	acc	atc	ttc	ttc	gcg	gct	ctg	ttg	atg	aac	ctt	gca	451	
Pro	Ile	Leu	Ala	Thr	Ile	Phe	Phe	Ala	Ala	Leu	Leu	Met	Asn	Leu	Ala		
			105					110					115				
acg	atc	atc	ccg	gga	cta	aac	atc	tcc	tcc	aac	tca	cgt	att	gca	ttc	499	
Thr	Ile	Ile	Pro	Gly	Leu	Asn	Ile	Ser	Ser	Asn	Ser	Arg	Ile	Ala	Phe		
		120					125					130					
cca	atc	gtg	atg	gcg	gta	gct	ggg	tac	atc	gcg	ttt	atc	tac	gca	ggc	547	
Pro	Ile	Val	Met	Ala	Val	Ala	Gly	Tyr	Ile	Ala	Phe	Ile	Tyr	Ala	Gly		
		135				140					145						
tct	aag	cgt	tac	gga	ttc	ttc	aaa	tat	gtg	aag	tct	tct	ggt	gtg	att	595	
Ser	Lys	Arg	Tyr	Gly	Phe	Phe	Lys	Tyr	Val	Lys	Ser	Ser	Val	Val	Ile		
		150			155					160					165		
ccg	aac	att	cca	cca	gca	ctt	cac	gtc	ttg	gtg	ggt	cca	att	gag	ttc	643	
Pro	Asn	Ile	Pro	Pro	Ala	Leu	His	Val	Leu	Val	Val	Pro	Ile	Glu	Phe		
				170					175					180			
ttc	tct	aca	ttc	atc	ttg	agg	cca	gtc	acc	ctg	gca	ctg	cgt	ttg	atg	691	
Phe	Ser	Thr	Phe	Ile	Leu	Arg	Pro	Val	Thr	Leu	Ala	Leu	Arg	Leu	Met		
			185					190					195				
gcc	aac	ttc	ctt	gct	ggc	cac	atc	atc	ctg	ggt	ctg	ctt	ttc	ttc	gca	739	
Ala	Asn	Phe	Leu	Ala	Gly	His	Ile	Ile	Leu	Val	Leu	Leu	Phe	Phe	Ala		
		200					205					210					
acg	aac	ttc	ttc	ttc	ttc	cag	ttc	aac	gga	tgg	aca	gca	atg	tcc	ggc	787	
Thr	Asn	Phe	Phe	Phe	Phe	Gln	Phe	Asn	Gly	Trp	Thr	Ala	Met	Ser	Gly		
		215				220					225						
gta	acc	atc	ttg	atg	gca	gta	ctc	ttc	acg	ggt	tac	gag	atc	att	ggt	835	
Val	Thr	Ile	Leu	Met	Ala	Val	Leu	Phe	Thr	Val	Tyr	Glu	Ile	Ile	Val		
		230			235					240					245		
atc	ttc	ctg	cag	gca	tac	atc	ttc	gct								862	
Ile	Phe	Leu	Gln	Ala	Tyr	Ile	Phe	Ala									
				250													

<210> 758

<211> 254

<212> PRT

<213> Corynebacterium glutamicum

<400> 758

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Met Lys Gly Glu Phe His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro
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Gly His Val Thr Asp Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp
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Phe Ala Asn Gly Trp Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu
          35           40           45

Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys
          50           55           60

Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu
          65           70           75           80

Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys
          85           90           95

Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu
          100          105          110

Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn
          115          120          125

Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala
          130          135          140

Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys
          145          150          155          160

Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val
          165          170          175

Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu
          180          185          190

Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val
          195          200          205

Leu Leu Phe Phe Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp
          210          215          220

Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val
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Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala
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<210> 759

<211> 1764

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1741)

<223> RXA01201

<400> 759

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attagtaatg ctggaagaaa caaccgagag caggaagaac atg gcg gag ctg acg 115
Met Ala Glu Leu Thr
1 5

atc tcc tcc gat gag atc cgt agc gcg att gcg aac tac acc tcg agc 163
Ile Ser Ser Asp Glu Ile Arg Ser Ala Ile Ala Asn Tyr Thr Ser Ser
10 15 20

tac tcc gcg gag gcc tcc cgt gag gag gtc ggc gtg gtt att tcg gcc 211
Tyr Ser Ala Glu Ala Ser Arg Glu Glu Val Gly Val Val Ile Ser Ala
25 30 35

gct gac ggt atc gcc cag gtt tcg ggc ctc ccg tca gta atg gcg aat 259
Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro Ser Val Met Ala Asn
40 45 50

gag ctc ctc gaa ttc ccg ggc ggc gtc atc ggc gtc gca cag aac ctt 307
Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly Val Ala Gln Asn Leu
55 60 65

gaa gct gac cga gtc ggc gtc gtg gtc ctg ggt aac tac gag cta ctt 355
Glu Ala Asp Arg Val Gly Val Val Val Leu Gly Asn Tyr Glu Leu Leu
70 75 80 85

aaa gaa ggc gac caa gtt cgt cgt act gga gac gtt ctg tct atc cca 403
Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp Val Leu Ser Ile Pro
90 95 100

gtc ggc gag gca ttc ctt ggc cgc gtt atc aac ccc ctt ggc cag cca 451
Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn Pro Leu Gly Gln Pro
105 110 115

att gac ggc ctg ggc gaa att gca tcc gaa gag gac cgc gtc ctc gag 499
Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu Asp Arg Val Leu Glu
120 125 130

ctt cag gca cca acc gtg ctt gag cgc cag cct gtc gag gag cct ttg 547
Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro Val Glu Glu Pro Leu
135 140 145

gca acc ggc atc aag gct atc gat gca atg acc cca atc ggc cgc ggt 595
Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr Pro Ile Gly Arg Gly
150 155 160 165

cag cgt cag ctg atc att ggt gac cgt aag act ggc aag acc gca gtc 643
Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr Gly Lys Thr Ala Val
170 175 180

tgt gtc gat acc atc ctt aac cag aag gcc aac tgg gag acc ggc gac 691
Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn Trp Glu Thr Gly Asp
185 190 195

aag acc aag cag gtt cgc tgc atc tac gtc gca atc ggt cag aag ggc 739
Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala Ile Gly Gln Lys Gly
200 205 210

tcc acc att gca gcc ctg cgt aag acc ctc gag gag cag ggc gct ctc 787
Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu Glu Gln Gly Ala Leu
215 220 225

gag tac acc acc atc gtg gct gca ccc gct tcc gat gct gca ggc ttc	835
Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser Asp Ala Ala Gly Phe	
230 235 240 245	
aag tgg ctt gca cca ttc gct ggc gct gct ctc gcc cag cac tgg atg	883
Lys Trp Leu Ala Pro Phe Ala Gly Ala Leu Ala Gln His Trp Met	
250 255 260	
tac cag ggc aac cac gtc ctg gtc atc tac gat gat ctg acc aag cag	931
Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp Asp Leu Thr Lys Gln	
265 270 275	
gct gag gca tac cgt gct atc tcc ctg ctg ctg cgt cgc cca ccg ggc	979
Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly	
280 285 290	
cgc gaa gca tac cca ggt gac gtc ttc tac ctg cac tcc cgt ctg ctg	1027
Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu	
295 300 305	
gag cgc gct gcg aag ctg tcc gat gaa cta ggc gca ggt tct att aca	1075
Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly Ala Gly Ser Ile Thr	
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gca ctg cca atc att gag acc aag gct aat gac gtt tcc gcc ttc att	1123
Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp Val Ser Ala Phe Ile	
330 335 340	
cct acc aac gtg att tcc atc acc gac ggt cag gta ttc ctt gag tcc	1171
Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln Val Phe Leu Glu Ser	
345 350 355	
gac ctg ttc aac cgt ggc gtt cgc ccg gcg atc aac gtc ggt gta tcc	1219
Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile Asn Val Gly Val Ser	
360 365 370	
gtc tcc cgt gtc ggt ggc gca gct cag acc aag ggt atg aag aag gtt	1267
Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys Gly Met Lys Lys Val	
375 380 385	
gcc ggt tct ctc cgt ctg gat ctg gct gca ttc cgc gac ctg gaa gca	1315
Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe Arg Asp Leu Glu Ala	
390 395 400 405	
ttc gct acc ttc gca tct gac ttg gat gct gca tcc aag tct cag ctt	1363
Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala Ser Lys Ser Gln Leu	
410 415 420	
gag cgt ggc cag cgc ctc gtt cag ctg ttg att cag tct gag aac gca	1411
Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile Gln Ser Glu Asn Ala	
425 430 435	
cct cag gct gtt gag tac cag atc att tct ctc tgg ctt gca ggc gaa	1459
Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu Trp Leu Ala Gly Glu	
440 445 450	
ggc gca ttc gac aac gtt cct gtt gaa gat gtt cgt cgc ttc gag tcc	1507
Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val Arg Arg Phe Glu Ser	
455 460 465	

gaa ctg cac gag tac tta ggc tcc aac gct gca cag gtc tac gag cag 1555
 Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala Gln Val Tyr Glu Gln
 470 475 480 485

 atc gct ggt gga gct cag ctt tcc gac gag tcc aag gaa acc ttg ctc 1603
 Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser Lys Glu Thr Leu Leu
 490 495 500

 aag gca acc gaa gat ttc aag agc gct ttc cag acc acc gat ggc acc 1651
 Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln Thr Thr Asp Gly Thr
 505 510 515

 cct gtc atc aac gag cct gag gtt gaa gca ctc gat gca ggc cag gtc 1699
 Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu Asp Ala Gly Gln Val
 520 525 530

 aag aaa gac cag ctc acc gtt tcc cgc aag gtc agc aag aag 1741
 Lys Lys Asp Gln Leu Thr Val Ser Arg Lys Val Ser Lys Lys
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 taaggcagcg agcctacact aaa 1764

<210> 760
 <211> 547
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Val Val Ile Ser Ala Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro
 35 40 45

 Ser Val Met Ala Asn Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly
 50 55 60

 Val Ala Gln Asn Leu Glu Ala Asp Arg Val Gly Val Val Val Leu Gly
 65 70 75 80

 Asn Tyr Glu Leu Leu Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp
 85 90 95

 Val Leu Ser Ile Pro Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn
 100 105 110

 Pro Leu Gly Gln Pro Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu
 115 120 125

 Asp Arg Val Leu Glu Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro
 130 135 140

 Val Glu Glu Pro Leu Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
 145 150 155 160

 Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
 165 170 175

Gly Lys Thr Ala Val Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn
 180 185 190
 Trp Glu Thr Gly Asp Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala
 195 200 205
 Ile Gly Gln Lys Gly Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu
 210 215 220
 Glu Gln Gly Ala Leu Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser
 225 230 235 240
 Asp Ala Ala Gly Phe Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu
 245 250 255
 Ala Gln His Trp Met Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp
 260 265 270
 Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu
 275 280 285
 Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu
 290 295 300
 His Ser Arg Leu Leu Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly
 305 310 315 320
 Ala Gly Ser Ile Thr Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp
 325 330 335
 Val Ser Ala Phe Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln
 340 345 350
 Val Phe Leu Glu Ser Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile
 355 360 365
 Asn Val Gly Val Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys
 370 375 380
 Gly Met Lys Lys Val Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe
 385 390 395 400
 Arg Asp Leu Glu Ala Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala
 405 410 415
 Ser Lys Ser Gln Leu Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile
 420 425 430
 Gln Ser Glu Asn Ala Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu
 435 440 445
 Trp Leu Ala Gly Glu Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val
 450 455 460
 Arg Arg Phe Glu Ser Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala
 465 470 475 480
 Gln Val Tyr Glu Gln Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser
 485 490 495

Lys Glu Thr Leu Leu Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln
500 505 510

Thr Thr Asp Gly Thr Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu
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Ser Lys Lys
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<210> 761

<211> 1572

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (1549)

<223> RXN01193

<400> 761

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Met Thr Thr Ala Leu
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gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt 163
Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg
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gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211
Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro
25 30 35

gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259
Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys
40 45 50

aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307
Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile
55 60 65

cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355
 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala
 70 75 80 85

gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403
Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val
90 95 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451
Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser
105 110 115

ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca 499
Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro
120 125 130

cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc	547
Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly	
135 140 145	
atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc	595
Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile	
150 155 160 165	
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Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu	
170 175 180	
atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca	691
Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala	
185 190 195	
ggt gtt ggt gag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg	739
Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met	
200 205 210	
gaa gaa atg ggc gtt ctc cag gac acc gcc ctg gtg ttc ggt cag atg	787
Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu Val Phe Gly Gln Met	
215 220 225	
gat gag cca cca gga gtc ggt atg cgc gtg gct ctg tcc ggc ctg acc	835
Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala Leu Ser Gly Leu Thr	
230 235 240 245	
atg gcg gag tac ttc cgc gat gtt cag aac cag gac gtg ctg ctg ttc	883
Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe	
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atc gac aac atc ttc cgt ttc acc cag gca ggt tct gag gtt tcc acc	931
Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr	
265 270 275	
ctt ctg ggt cgt atg cct tcc gcc gtg ggt tac cag cca acc ctg gct	979
Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala	
280 285 290	
gac gag atg ggt gtt ctc cag gag cgc att acc tcc acc aag ggc cgt	1027
Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg	
295 300 305	
tcg att acc tct ctg cag gcc gtt tac gtt cct gcc gat gac tac acc	1075
Ser Ile Thr Ser Leu Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr	
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Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu	
330 335 340	
ctt gac cgc tcc att gct tcc aag ggt att tac cca gca gtg aac cca	1171
Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro	
345 350 355	
ctg acc tcc acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt	1219
Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg	
360 365 370	

cac tac gag gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag 1267
 His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys
 375 380 385

 gaa ctt cag gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa 1315
 Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu
 390 395 400 405

 gag gac aag atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg 1363
 Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu
 410 415 420

 ggt cag aac ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc 1411
 Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser
 425 430 435

 tac gtg cca ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac 1459
 Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn
 440 445 450

 ggc gac ttc gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt 1507
 Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly
 455 460 465

 ttg gac gat gtc gaa gct gca tac aag aag ctg acc gga aag 1549
 Leu Asp Asp Val Glu Ala Ala Tyr Lys Lys Leu Thr Gly Lys
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 taaggtagag acacatggct gaa 1572

<210> 762

<211> 483

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 762

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 Gly Arg Val Val Arg Val Ile Gly Ala Val Val Asp Val Glu Phe Pro
 20 25 30

 Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr
 35 40 45

 Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu
 50 55 60

 Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu
 65 70 75 80

 Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro
 85 90 95

 Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys
 100 105 110

 Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly
 115 120 125

Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu
 130 135 140
 Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val
 145 150 155 160
 Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr
 165 170 175
 Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly
 180 185 190
 Thr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp
 195 200 205
 Leu Phe Leu Glu Met Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu
 210 215 220
 Val Phe Gly Gln Met Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala
 225 230 235 240
 Leu Ser Gly Leu Thr Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln
 245 250 255
 Asp Val Leu Leu Phe Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly
 260 265 270
 Ser Glu Val Ser Thr Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr
 275 280 285
 Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr
 290 295 300
 Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala Val Tyr Val Pro
 305 310 315 320
 Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu
 325 330 335
 Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr
 340 345 350
 Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala
 355 360 365
 Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile
 370 375 380
 Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met
 385 390 395 400
 Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg
 405 410 415
 Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr
 420 425 430
 Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe
 435 440 445
 Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe

450 455 460
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 465 470 475 480
 Thr Gly Lys

 <210> 763
 <211> 778
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
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 <222> (15)..(755)
 <223> FRXA01193

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 tac ttc cgc gat gtt cag aac cag gac gtg ctg ctg ttc atc gac aac 98
 Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn
 15 20 25

 atc ttc cgt ttc acc cag gca ggt tct gag gtt tcc acc ctt ctg ggt 146
 Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly
 30 35 40

 cgt atg cct tcc gcc gtg ggt tac cag cca acc ctg gct gac gag atg 194
 Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met
 45 50 55 60

 ggt gtt ctc cag gag cgc att acc tcc acc aag ggc cgt tcg att acc 242
 Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg Ser Ile Thr
 65 70 75

 tct ctg cag gcc gtt tac gtt cct gcc gat gac tac acc gac ccg gct 290
 Ser Leu Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala
 80 85 90

 cca gcg acc acc ttc gct cac ttg gat gca acc acc gag ctt gac cgc 338
 Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg
 95 100 105

 tcc att gct tcc aag ggt att tac cca gca gtg aac cca ctg acc tcc 386
 Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser
 110 115 120

 acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt cac tac gag 434
 Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu
 125 130 135 140

 gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag gaa ctt cag 482
 Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln
 145 150 155

 gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa gag gac aag 530

Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys
 160 165 170
 atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg ggt cag aac 578
 Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn
 175 180 185
 ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc tac gtg cca 626
 Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro
 190 195 200
 ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac ggc gac ttc 674
 Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe
 205 210 215 220
 gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt ttg gac gat 722
 Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly Leu Asp Asp
 225 230 235
 gtc gaa gct gca tac aag aag ctg acc gga aag taaggtagag acacatggct 775
 Val Glu Ala Ala Tyr Lys Lys Leu Thr Gly Lys
 240 245
 gaa 778

<210> 764
 <211> 247
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 764
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 Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met Pro Ser
 35 40 45
 Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln
 50 55 60
 Glu Arg Ile Thr Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala
 65 70 75 80
 Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr
 85 90 95
 Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser
 100 105 110
 Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile
 115 120 125
 Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg
 130 135 140
 Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala
 145 150 155 160

Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala
 165 170 175

Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala
 180 185 190

Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr
 195 200 205

Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro
 210 215 220

Glu Gln Ala Phe Asn Gly Leu Gly Gly Leu Asp Asp Val Glu Ala Ala
 225 230 235 240

Tyr Lys Lys Leu Thr Gly Lys
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<210> 765
 <211> 739
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(739)
 <223> FRXA01203

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gcgcaggcgc gctcgccgac agcggagaaa gtgactaatt atg act aca gct ctt 115
 Met Thr Thr Ala Leu
 1 5

gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt 163
 Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg
 10 15 20

gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211
 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro
 25 30 35

gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259
 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys
 40 45 50

aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307
 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile
 55 60 65

cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355
 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala
 70 75 80 85

gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403
 Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val
 90 95 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451
 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser
 105 110 115
 ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca 499
 Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro
 120 125 130
 cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc 547
 Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly
 135 140 145
 atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc 595
 Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
 150 155 160 165
 ggc ctc ttc ggt ggt gca ggt gtg ggt aag acc gtt ctt atc cag gaa 643
 Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu
 170 175 180
 atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca 691
 Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala
 185 190 195
 ggt gtt ggt aag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg 739
 Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met
 200 205 210

<210> 766

<211> 213

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 766

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 20 25 30
 Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr
 35 40 45
 Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu
 50 55 60
 Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu
 65 70 75 80
 Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro
 85 90 95
 Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys
 100 105 110
 Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly
 115 120 125
 Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu
 130 135 140

Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val
 145 150 155 160
 Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr
 165 170 175
 Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly
 180 185 190
 Thr Ser Val Phe Ala Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp
 195 200 205
 Leu Phe Leu Glu Met
 210

<210> 767
 <211> 363
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(340)
 <223> RXN02821

<400> 767
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 cagcccgaac acacggggcac cagaaaggga acgacacctc atg aac gag atc atc 115
 Met Asn Glu Ile Ile
 1 5
 ctg gca cag gac gca acc gag tcc acc atc acc gga ctt ggc gct gtc 163
 Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr Gly Leu Gly Ala Val
 10 15 20
 ggc tac ggc atc gca acc atc gga cct ggc ctc ggc atc ggc atc ctg 211
 Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu
 25 30 35
 gtt ggt aag gct ctc gag ggt atg gca cgt cag cct gag atg gct gga 259
 Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly
 40 45 50
 cag ctc cgt acc acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg 307
 Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu
 55 60 65
 gca ctg atc ggc ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga 360
 Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
 70 75 80
 aag 363

<210> 768
 <211> 80
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 768

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Met Asn Glu Ile Ile Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr
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Gly Leu Gly Ala Val Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu
          20             25             30

Gly Ile Gly Ile Leu Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln
          35             40             45

Pro Glu Met Ala Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala
 50             55             60

Phe Val Glu Ala Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
65             70             75             80

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<210> 769

<211> 303

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(280)

<223> FRXA02821

<400> 769

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caggacgcaa ccgagtccac catcaccgga ccttggcgct gtg ggc tac ggc atc 115
                               Val Gly Tyr Gly Ile
                               1             5

gca acc atc gga cct ggc ctc ggc atc ggc atc ttg gtt ggt aag gct 163
Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu Val Gly Lys Ala
          10             15             20

ctc gag ggt atg gca cgt cag cct gag atg gct gga cag ctc cgt acc 211
Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly Gln Leu Arg Thr
          25             30             35

acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg gca ctg atc ggc 259
Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu Ala Leu Ile Gly
          40             45             50

ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga aag 303
Leu Val Ala Gly Phe Leu Phe
          55             60

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<210> 770

<211> 60

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 770

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 Leu Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala
 20 25 30
 Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala
 35 40 45
 Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
 50 55 60

<210> 771

<211> 632

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(609)

<223> RXA01200

<400> 771

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 Gly Cys Leu Arg Trp Lys Ser Glu Pro Ser Val Leu Glu Val Leu Lys
 1 5 10 15
 gac gcc gca gag cag acc tgg tcc act cca cgc gag ttc cgc gct gga 96
 Asp Ala Ala Glu Gln Thr Trp Ser Thr Pro Arg Glu Phe Arg Ala Gly
 20 25 30
 cta gtc caa ctt ggc cgt cgc gcc ctt ctt cgc tct gcg gag aaa cag 144
 Leu Val Gln Leu Gly Arg Arg Ala Leu Leu Arg Ser Ala Glu Lys Gln
 35 40 45
 ggt cag ctt ggt cag gtg gaa gat gaa ctg ttc cga ctc agc cga atc 192
 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile
 50 55 60
 ctg gat cgc gaa agc aag ctg act cag ctt ctt tca gat cgc act cag 240
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln
 65 70 75 80
 gaa att ggc ggt cga cgt gac ctc ctg gct aag gtg ctc tac ggc aag 288
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys
 85 90 95
 gta act gct gtt acc gaa gcc ctc gca ctg cag gct att ggt cgc cct 336
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro
 100 105 110
 gag cac aac cca att gac gat atc gca gct ttg gct ggc gct gta gca 384
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala
 115 120 125
 gag cta cag ggt cgt tcc gtt gca cat gtc gtt acc gca gtt gaa ctc 432
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu
 130 135 140
 aac gag gga cag caa caa gcg cta gct gaa aag ctg gga cgt att tat 480

Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr
 145 150 155 160
 ggt cgt gcg atg agc atc cac tcc gag gtt gat acc agc ctc ctc ggt 528
 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly
 165 170 175
 gga atg atc atc cgc gtc gga gac gaa gta att gac ggc agc acc tcg 576
 Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser
 180 185 190
 ggc aaa ctc gag cgt ctg cgg gca agc ttc gca taaagacacg acgaattaga 629
 Gly Lys Leu Glu Arg Leu Arg Ala Ser Phe Ala
 195 200
 caa 632
 <210> 772
 <211> 203
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 772
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 35 40 45
 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile
 50 55 60
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln
 65 70 75 80
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys
 85 90 95
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro
 100 105 110
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala
 115 120 125
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu
 130 135 140
 Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr
 145 150 155 160
 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly
 165 170 175
 Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser
 180 185 190
 Gly Lys Leu Glu Arg Leu Arg Ala Ser Phe Ala

200

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<223> RXA01194
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<211> 124
<212> PRT
<213> Corynebacterium glutamicum
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			20					25					30		
Gly	Val	Leu	Pro	Asp	His	Glu	Pro	Leu	Leu	Gly	Gln	Leu	Val	Glu	Asn
		35					40					45			
Gly	Val	Val	Thr	Ile	Gln	Pro	Ile	Asp	Gly	Glu	Lys	Leu	Ile	Ala	Gly
	50					55					60				
Val	Ser	Asp	Gly	Phe	Leu	Ser	Val	Ser	Lys	Glu	Lys	Val	Thr	Ile	Leu
65					70					75					80
Ala	Asp	Phe	Ala	Val	Trp	Ala	Asn	Glu	Val	Asp	Thr	Ala	Ser	Ala	Glu
				85					90					95	
Ala	Asp	Leu	Asn	Ser	Asp	Asp	Glu	Leu	Ala	Lys	Ala	His	Ala	Glu	Ala
			100					105					110		
Gly	Leu	Arg	Ala	Val	Arg	Arg	Ser	Ser	Glu	Gly	Leu				
		115					120								

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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1075)  
<223> RXA01202
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				atg	gca	aca	att	cgt								
				Met	Ala	Thr	Ile	Arg								
				1					5							
gaa ttg cgt gac cga att cgt tcg gtt aac tca acc aag aag atc acc															163	
Glu	Leu	Arg	Asp	Arg	Ile	Arg	Ser	Val	Asn	Ser	Thr	Lys	Lys	Ile	Thr	
				10					15					20		
aag gct caa gag ctc atc gcc acc tct cgc atc acc aag gca cag ggt															211	
Lys	Ala	Gln	Glu	Leu	Ile	Ala	Thr	Ser	Arg	Ile	Thr	Lys	Ala	Gln	Gly	
				25					30					35		
cgc gtc gcg gca gct gcg ccg tac gcc gag gaa atc cag cgc gtg ctg															259	
Arg	Val	Ala	Ala	Ala	Ala	Pro	Tyr	Ala	Glu	Glu	Ile	Gln	Arg	Val	Leu	
				40					45					50		
gag cgc ctc gcg tcg gca agc tcc cta gac cac cca atg ctg cgt gag															307	
Glu	Arg	Leu	Ala	Ser	Ala	Ser	Ser	Leu	Asp	His	Pro	Met	Leu	Arg	Glu	
				55					60					65		
cgt gaa ggc ggc aag cga gcc gcc gtg ctc gtg gtt act tct gac cgc															355	
Arg	Glu	Gly	Gly	Lys	Arg	Ala	Ala	Val	Leu	Val	Val	Thr	Ser	Asp	Arg	
				70					75					80	85	
ggc atg gct ggt ggc tac aac cac aac gtt ctg aaa aag gca gcg gag															403	

Gly	Met	Ala	Gly	Gly	Tyr	Asn	His	Asn	Val	Leu	Lys	Lys	Ala	Ala	Glu		
				90					95						100		
ctg	gaa	aag	ctt	ctt	gct	gaa	agt	gga	tac	gaa	gtg	gtt	cgt	tat	gtc	451	
Leu	Glu	Lys	Leu	Leu	Ala	Glu	Ser	Gly	Tyr	Glu	Val	Val	Arg	Tyr	Val		
			105					110					115				
acc	ggc	aaa	aag	ggc	gtc	gac	tac	tac	aag	ttc	cgc	gct	gaa	gat	gtg	499	
Thr	Gly	Lys	Lys	Gly	Val	Asp	Tyr	Tyr	Lys	Phe	Arg	Ala	Glu	Asp	Val		
			120				125					130					
gct	ggc	acc	tgg	act	gga	ttc	tca	cag	gat	cca	gac	tgg	gca	gct	acc	547	
Ala	Gly	Thr	Trp	Thr	Gly	Phe	Ser	Gln	Asp	Pro	Asp	Trp	Ala	Ala	Thr		
			135				140				145						
cac	aac	gtg	cgc	cgt	cac	ctc	att	gat	ggg	ttc	acc	gcc	agc	tct	gaa	595	
His	Asn	Val	Arg	Arg	His	Leu	Ile	Asp	Gly	Phe	Thr	Ala	Ser	Ser	Glu		
						155				160					165		
ggg	gaa	gct	gca	tgg	cgc	gag	gga	ctg	aac	cta	cca	gaa	ggc	cag	gat	643	
Gly	Glu	Ala	Ala	Trp	Arg	Glu	Gly	Leu	Asn	Leu	Pro	Glu	Gly	Gln	Asp		
				170					175					180			
atc	cag	ggc	ttc	gac	cag	gtt	cac	gtg	gtc	tac	acc	gag	ttc	atc	tcc	691	
Ile	Gln	Gly	Phe	Asp	Gln	Val	His	Val	Val	Tyr	Thr	Glu	Phe	Ile	Ser		
			185					190					195				
atg	ctg	act	caa	aac	cca	gta	gtg	cac	caa	ctg	ctg	cct	gtt	gag	cca	739	
Met	Leu	Thr	Gln	Asn	Pro	Val	Val	His	Gln	Leu	Leu	Pro	Val	Glu	Pro		
			200				205					210					
gtc	atc	gaa	gat	gaa	att	ttc	gaa	aaa	ggc	gag	gat	ctg	ctg	tcc	tct	787	
Val	Ile	Glu	Asp	Glu	Ile	Phe	Glu	Lys	Gly	Glu	Asp	Leu	Leu	Ser	Ser		
			215				220				225						
tcc	ggc	gaa	gtc	gaa	ccc	gac	tac	gag	ttc	gag	ccg	gat	gca	gac	act	835	
Ser	Gly	Glu	Val	Glu	Pro	Asp	Tyr	Glu	Phe	Glu	Pro	Asp	Ala	Asp	Thr		
						235				240					245		
ctg	ctt	gag	gca	ctg	ctt	ccg	cag	tac	gtc	tct	cgt	agg	ctg	ttc	tcc	883	
Leu	Leu	Glu	Ala	Leu	Leu	Pro	Gln	Tyr	Val	Ser	Arg	Arg	Leu	Phe	Ser		
				250					255					260			
atc	ttc	ttg	gag	gct	gca	gct	gca	gag	tcc	gct	tca	cgt	cga	aac	gcg	931	
Ile	Phe	Leu	Glu	Ala	Ala	Ala	Ala	Glu	Ser	Ala	Ser	Arg	Arg	Asn	Ala		
				265				270					275				
atg	aag	tct	gcg	act	gac	aac	gct	acg	gaa	ctg	gtc	aag	gac	ctg	tcc	979	
Met	Lys	Ser	Ala	Thr	Asp	Asn	Ala	Thr	Glu	Leu	Val	Lys	Asp	Leu	Ser		
			280				285					290					
cgt	gtg	gcc	aac	cag	gca	cgt	cag	gca	cag	atc	acc	cag	gaa	atc	aca	1027	
Arg	Val	Ala	Asn	Gln	Ala	Arg	Gln	Ala	Gln	Ile	Thr	Gln	Glu	Ile	Thr		
			295				300				305						
gag	att	gtt	ggg	ggc	gca	ggc	gcg	ctc	gcc	gac	agc	gga	gaa	agt	gac	1075	
Glu	Ile	Val	Gly	Gly	Ala	Gly	Ala	Leu	Ala	Asp	Ser	Gly	Glu	Ser	Asp		
					315				320						325		
taattatgac	tacagctctt	gaa														1098	

<210> 776

<211> 325

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 776

Met Ala Thr Ile Arg Glu Leu Arg Asp Arg Ile Arg Ser Val Asn Ser
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Thr Lys Lys Ile Thr Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile
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Thr Lys Ala Gln Gly Arg Val Ala Ala Ala Ala Pro Tyr Ala Glu Glu
 35 40 45

Ile Gln Arg Val Leu Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His
 50 55 60

Pro Met Leu Arg Glu Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val
 65 70 75 80

Val Thr Ser Asp Arg Gly Met Ala Gly Gly Tyr Asn His Asn Val Leu
 85 90 95

Lys Lys Ala Ala Glu Leu Glu Lys Leu Leu Ala Glu Ser Gly Tyr Glu
 100 105 110

Val Val Arg Tyr Val Thr Gly Lys Lys Gly Val Asp Tyr Tyr Lys Phe
 115 120 125

Arg Ala Glu Asp Val Ala Gly Thr Trp Thr Gly Phe Ser Gln Asp Pro
 130 135 140

Asp Trp Ala Ala Thr His Asn Val Arg Arg His Leu Ile Asp Gly Phe
 145 150 155 160

Thr Ala Ser Ser Glu Gly Glu Ala Ala Trp Arg Glu Gly Leu Asn Leu
 165 170 175

Pro Glu Gly Gln Asp Ile Gln Gly Phe Asp Gln Val His Val Val Tyr
 180 185 190

Thr Glu Phe Ile Ser Met Leu Thr Gln Asn Pro Val Val His Gln Leu
 195 200 205

Leu Pro Val Glu Pro Val Ile Glu Asp Glu Ile Phe Glu Lys Gly Glu
 210 215 220

Asp Leu Leu Ser Ser Ser Gly Glu Val Glu Pro Asp Tyr Glu Phe Glu
 225 230 235 240

Pro Asp Ala Asp Thr Leu Leu Glu Ala Leu Leu Pro Gln Tyr Val Ser
 245 250 255

Arg Arg Leu Phe Ser Ile Phe Leu Glu Ala Ala Ala Ala Glu Ser Ala
 260 265 270

Ser Arg Arg Asn Ala Met Lys Ser Ala Thr Asp Asn Ala Thr Glu Leu
 275 280 285

Val Lys Asp Leu Ser Arg Val Ala Asn Gln Ala Arg Gln Ala Gln Ile
 290 295 300

Thr Gln Glu Ile Thr Glu Ile Val Gly Gly Ala Gly Ala Leu Ala Asp
 305 310 315 320

Ser Gly Glu Ser Asp
 325

<210> 777

<211> 1773

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1750)

<223> RXN02434

<400> 777

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tgtggcaggc cttgcgtttt gacattgaag gacccttttt atg cgc act ttt gcc 115
 Met Arg Thr Phe Ala
 1 5

gct tat att gcc att gat ggc ctc agc ttt tcc tac ccc aac acc cac 163
 Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser Tyr Pro Asn Thr His
 10 15 20

gtt tta agc gat att tcg ctc acc gtt gcc aat ggc gat atc gcc gga 211
 Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn Gly Asp Ile Ala Gly
 25 30 35

ctg att ggt gaa aac ggc gca gga aaa tcc acc ctg ctc age ctc atc 259
 Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Leu Ile
 40 45 50

gct ggc gtc atg gaa ccc gac cag ggc agg att tac ctc ccc gaa cgc 307
 Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile Tyr Leu Pro Glu Arg
 55 60 65

acc gga ttc atc gcc caa gaa aca gac tta ccg ttt gaa caa ccc gtg 355
 Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro Phe Glu Gln Pro Val
 70 75 80 85

cag tcg ctt atc gac gcc gcc gtc gcc cca gtg cgc gcg gtc gat gcc 403
 Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val Arg Ala Val Asp Ala
 90 95 100

gcg att aca gat ttg tcc acc aag ctt ggc gac gcc tcc ctc agc gcc 451
 Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp Ala Ser Leu Ser Ala
 105 110 115

gaa gag cag gcg caa gtc gcc aca gat ttc gat gca gcg cta ggc gct 499
 Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp Ala Ala Leu Gly Ala
 120 125 130

gca gaa gaa ctc gga ctg tgg gaa tta gat gca cgt att gaa acc atc 547
 Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala Arg Ile Glu Thr Ile

135	140	145	
gtc gcg ggt ctc ggc ctt gcc gag gtg gat cgc agc act ccc att ggt Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg Ser Thr Pro Ile Gly 150 155 160 165			595
gag ctt tcc ggc ggt cag cgc cgc aga ttc gca ttg gca gcg ctg ctg Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala Leu Ala Ala Leu Leu 170 175 180			643
ttg gaa cca cac gat gct ctg att ttc gat gag ccc acc aac cac ctc Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu Pro Thr Asn His Leu 185 190 195			691
gac gac aca gcc gta gat ttc ctc atc tcg gag att tcc cgt ttc aaa Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu Ile Ser Arg Phe Lys 200 205 210			739
ggg cca gtg ctg atc gcc agc cac gat cgc ttc ttc ctc gac tcc gtc Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe Phe Leu Asp Ser Val 215 220 225			787
tgt acc gag tta atc gac ctc gat cct gca ctt gga cct gag ggc gga Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu Gly Pro Glu Gly Gly 230 235 240 245			835
tcc ggc gaa gaa gta aaa caa gcc gtg tct ttt ggt ggt gga ttt tct Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe Gly Gly Gly Phe Ser 250 255 260			883
gaa tac atc aaa gaa cgc gag acc cgc cgc acc cgc tgg gct cag ttg Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr Arg Trp Ala Gln Leu 265 270 275			931
tac acc gca caa gaa acc gag cgg gaa aaa ctc gaa gaa acc acc ggc Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu Glu Glu Thr Thr Gly 280 285 290			979
acc acc gaa tcg gat att ttc cac agc tcg gtt tcc aaa tcg gaa gct Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val Ser Lys Ser Glu Ala 295 300 305			1027
aaa atc acc gcg aaa ttt tac gca gac cgg gca gct aaa act caa ggc Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala Ala Lys Thr Gln Gly 310 315 320 325			1075
aac cgc gtc cgc tcc gcc aaa aac cgc ctg aag gaa ttg gaa cgc tat Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys Glu Leu Glu Arg Tyr 330 335 340			1123
gaa atc cca gca cct cca aag cca ctg gaa ttc caa ggc atc cca gaa Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe Gln Gly Ile Pro Glu 345 350 355			1171
gcc tcc gga aac ggt cac ggt gaa aca cta gaa gtg cgg gct att gct Ala Ser Gly Asn Gly His Gly Glu Thr Leu Glu Val Arg Ala Ile Ala 360 365 370			1219
gtg gaa aac agg ctt caa ccc ttg act ttc cac atc gat ccc ggc gac Val Glu Asn Arg Leu Gln Pro Leu Thr Phe His Ile Asp Pro Gly Asp 375 380 385			1267

cac atc ctg gtc gaa ggc ccc aac ggt gtc ggt aaa tcc acc ctg ctg 1315
 His Ile Leu Val Glu Gly Pro Asn Gly Val Gly Lys Ser Thr Leu Leu
 390 395 400 405

 agc gtt ctg gaa ggc gtg ctt gaa cca acc gaa ggt gaa ttg atc gtc 1363
 Ser Val Leu Glu Gly Val Leu Glu Pro Thr Glu Gly Glu Leu Ile Val
 410 415 420

 ccc gaa ggg ctg aaa gtt gcg cgc ctg aaa cag gac gat cag tgg acg 1411
 Pro Glu Gly Leu Lys Val Ala Arg Leu Lys Gln Asp Asp Gln Trp Thr
 425 430 435

 gaa aag cag ttg aac acc ccc gtc gac gaa ctg ttc gcc gcc cta tcg 1459
 Glu Lys Gln Leu Asn Thr Pro Val Asp Glu Leu Phe Ala Ala Leu Ser
 440 445 450

 aaa ggt ccg gtc gga ctc aac ctc gtg gag atg ggg ctg ttg agg gag 1507
 Lys Gly Pro Val Gly Leu Asn Leu Val Glu Met Gly Leu Leu Arg Glu
 455 460 465

 acg tcg caa agc agc ccg cta cgg gcc cta tcg ctc ggc caa cgc cgg 1555
 Thr Ser Gln Ser Ser Pro Leu Arg Ala Leu Ser Leu Gly Gln Arg Arg
 470 475 480 485

 cgc gtc tcg ctc ggg ctc atc ctg gcg agc cca cca gat ctt ttg ctt 1603
 Arg Val Ser Leu Gly Leu Ile Leu Ala Ser Pro Pro Asp Leu Leu Leu
 490 495 500

 ctt gac gag ccc acc aac cac ctc tcc ctc gcg ctg agc gaa gaa ctc 1651
 Leu Asp Glu Pro Thr Asn His Leu Ser Leu Ala Leu Ser Glu Glu Leu
 505 510 515

 gag tcg gcg ata gaa aaa ttc ccc ggt cgc gtt att ctg gcc agc cac 1699
 Glu Ser Ala Ile Glu Lys Phe Pro Gly Arg Val Ile Leu Ala Ser His
 520 525 530

 gat agg tgg atc aga aaa cgt tgg acg ggg aag aaa atc agc ctg agc 1747
 Asp Arg Trp Ile Arg Lys Arg Trp Thr Gly Lys Lys Ile Ser Leu Ser
 535 540 545

 cgt taaaccctac tgaacaggaa cct 1773
 Arg
 550

<210> 778

<211> 550

<212> PRT

<213> Corynebacterium glutamicum

<400> 778

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Tyr Pro Asn Thr His Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn
 20 25 30

Gly Asp Ile Ala Gly Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr
 35 40 45

Leu Leu Ser Leu Ile Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile
 50 55 60
 Tyr Leu Pro Glu Arg Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro
 65 70 75 80
 Phe Glu Gln Pro Val Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val
 85 90 95
 Arg Ala Val Asp Ala Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp
 100 105 110
 Ala Ser Leu Ser Ala Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp
 115 120 125
 Ala Ala Leu Gly Ala Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala
 130 135 140
 Arg Ile Glu Thr Ile Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg
 145 150 155 160
 Ser Thr Pro Ile Gly Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala
 165 170 175
 Leu Ala Ala Leu Leu Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu
 180 185 190
 Pro Thr Asn His Leu Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu
 195 200 205
 Ile Ser Arg Phe Lys Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe
 210 215 220
 Phe Leu Asp Ser Val Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu
 225 230 235 240
 Gly Pro Glu Gly Gly Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe
 245 250 255
 Gly Gly Gly Phe Ser Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr
 260 265 270
 Arg Trp Ala Gln Leu Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu
 275 280 285
 Glu Glu Thr Thr Gly Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val
 290 295 300
 Ser Lys Ser Glu Ala Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala
 305 310 315 320
 Ala Lys Thr Gln Gly Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys
 325 330 335
 Glu Leu Glu Arg Tyr Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe
 340 345 350
 Gln Gly Ile Pro Glu Ala Ser Gly Asn Gly His Gly Glu Thr Leu Glu
 355 360 365
 Val Arg Ala Ile Ala Val Glu Asn Arg Leu Gln Pro Leu Thr Phe His

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<210> 779
<211> 1407
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101) .. (1384)  
<223> RXN00684
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gtgatcggtc tcggccacac acaagtgtca ggagatgaca atg act tcc cag act 115
Met Thr Ser Gln Thr
1 5
tcc caa caa tcc acc tca acc ggt gga tgc cca ttc ggg cac aca tca 163
Ser Gln Gln Ser Thr Ser Thr Gly Gly Cys Pro Phe Gly His Thr Ser
10 15 20
gag tcc acc agc cat cac ggc tac cag cct ttc gat atg cac aac ccg 211
Glu Ser Thr Ser His His Gly Tyr Gln Pro Phe Asp Met His Asn Pro
25 30 35

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ttt cct gca tat aaa gaa ctc cgt cag gaa gag cca gtg atg ttc gat	259
Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu Pro Val Met Phe Asp	
40 45 50	
gag cgc atc ggc tac tgg gtg gta acc aaa tat gac gac atc aaa acc	307
Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr Asp Asp Ile Lys Thr	
55 60 65	
acc ttt gat gac tgg gaa aca ttc tcc tct gaa aat gca caa gcc cca	355
Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu Asn Ala Gln Ala Pro	
70 75 80 85	
gtc cgc aag cgt gga cct cag gca acc caa atc atg acc gat ggc ggc	403
Val Arg Lys Arg Gly Pro Gln Ala Thr Gln Ile Met Thr Asp Gly Gly	
90 95 100	
ttc act gca tac tcc gga tta tca gct cgt att cca cca gag cac acc	451
Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile Pro Pro Glu His Thr	
105 110 115	
cgc atc cgc gca atc gca caa aag gcc ttc acg cca cgc cgc tat aaa	499
Arg Ile Arg Ala Ile Ala Gln Lys Ala Phe Thr Pro Arg Arg Tyr Lys	
120 125 130	
gca ctc gaa cca gat atc cga gca atg gtg att gat cgt gtg gag aaa	547
Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile Asp Arg Val Glu Lys	
135 140 145	
atg ttg gcg aat gat caa cac gtc ggc gat atg gtg tca gat ctt gcc	595
Met Leu Ala Asn Asp Gln His Val Gly Asp Met Val Ser Asp Leu Ala	
150 155 160 165	
tac gac att cca acc atc acg atc ctg acg ctg atc ggt gca gat att	643
Tyr Asp Ile Pro Thr Ile Thr Ile Leu Thr Leu Ile Gly Ala Asp Ile	
170 175 180	
ttc atg gtg gtc acc tac aag cgg tgg tca gat tcc cgt gcg gcc atg	691
Phe Met Val Val Thr Tyr Lys Arg Trp Ser Asp Ser Arg Ala Ala Met	
185 190 195	
acc tgg ggc gat ctt agt gat gaa gag cag atc cca cac gca cac aat	739
Thr Trp Gly Asp Leu Ser Asp Glu Glu Gln Ile Pro His Ala His Asn	
200 205 210	
ttg gtt gag tac tgg cag gaa tgc caa cgc atg gta gct gat gca cat	787
Leu Val Glu Tyr Trp Gln Glu Cys Gln Arg Met Val Ala Asp Ala His	
215 220 225	
gca cac ggt ggc gac aac ctc acc gct gat cta gtg cga gca cag caa	835
Ala His Gly Gly Asp Asn Leu Thr Ala Asp Leu Val Arg Ala Gln Gln	
230 235 240 245	
gag ggt caa gaa atc acc gat cat gag att gct tct ttg ctg tac tcc	883
Glu Gly Gln Glu Ile Thr Asp His Glu Ile Ala Ser Leu Leu Tyr Ser	
250 255 260	
ctg ctt ttt gcg ggg cac gaa aca acc acc acg ttg atc tcc aat tgt	931
Leu Leu Phe Ala Gly His Glu Thr Thr Thr Leu Ile Ser Asn Cys	
265 270 275	
ttc cga gtt ctc ctc gat cat cca gag cag tgg caa gcc att cta gag	979

Phe Arg Val Leu Leu Asp His Pro Glu Gln Trp Gln Ala Ile Leu Glu
 280 285 290
 aat cca aaa ctg att cct gcg gca gtg gat gag gtc ttg cgg tac tcc 1027
 Asn Pro Lys Leu Ile Pro Ala Ala Val Asp Glu Val Leu Arg Tyr Ser
 295 300 305
 ggc tcg atc gtg ggg tgg cgt cga aaa gca tta aaa gac acc gag atc 1075
 Gly Ser Ile Val Gly Trp Arg Arg Lys Ala Leu Lys Asp Thr Glu Ile
 310 315 320 325
 ggc ggc gtt gcc att aag gaa ggc gat ggt gtt ctg ctg ctc atg ggt 1123
 Gly Gly Val Ala Ile Lys Glu Gly Asp Gly Val Leu Leu Leu Met Gly
 330 335 340
 tcc gcg aac cgc gat gaa gct cgc ttt gaa aat ggc gag gaa ttc gat 1171
 Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn Gly Glu Glu Phe Asp
 345 350 355
 atc agc cgc gct aat gcg cgc gag cac ctg tct ttt ggt ttc ggc atc 1219
 Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser Phe Gly Phe Gly Ile
 360 365 370
 cac tat tgc cta gga aac atg ctg gcc aaa ctt caa gcc aag atc tgt 1267
 His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu Gln Ala Lys Ile Cys
 375 380 385
 ctc gag gaa gtc acc agg ctt gtt cct tcc ctg cac ttg gtt gcg gac 1315
 Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu His Leu Val Ala Asp
 390 395 400 405
 aaa gct atc ggg ttc cgg gag aac ctc tcc ttc cgc gtc ccc act tct 1363
 Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe Arg Val Pro Thr Ser
 410 415 420
 gtt ccc gtg act tgg aac gct taacgcttta ttaaataagg aga 1407
 Val Pro Val Thr Trp Asn Ala
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<210> 780

<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 780

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 Phe Gly His Thr Ser Glu Ser Thr Ser His His Gly Tyr Gln Pro Phe
 20 25 30
 Asp Met His Asn Pro Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu
 35 40 45
 Pro Val Met Phe Asp Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr
 50 55 60
 Asp Asp Ile Lys Thr Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu
 65 70 75 80

Asn Ala Gln Ala Pro Val Arg Lys Arg Gly Pro Gln Ala Thr Gln Ile
 85 90 95
 Met Thr Asp Gly Gly Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile
 100 105 110
 Pro Pro Glu His Thr Arg Ile Arg Ala Ile Ala Gln Lys Ala Phe Thr
 115 120 125
 Pro Arg Arg Tyr Lys Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile
 130 135 140
 Asp Arg Val Glu Lys Met Leu Ala Asn Asp Gln His Val Gly Asp Met
 145 150 155 160
 Val Ser Asp Leu Ala Tyr Asp Ile Pro Thr Ile Thr Ile Leu Thr Leu
 165 170 175
 Ile Gly Ala Asp Ile Phe Met Val Val Thr Tyr Lys Arg Trp Ser Asp
 180 185 190
 Ser Arg Ala Ala Met Thr Trp Gly Asp Leu Ser Asp Glu Glu Gln Ile
 195 200 205
 Pro His Ala His Asn Leu Val Glu Tyr Trp Gln Glu Cys Gln Arg Met
 210 215 220
 Val Ala Asp Ala His Ala His Gly Gly Asp Asn Leu Thr Ala Asp Leu
 225 230 235 240
 Val Arg Ala Gln Gln Glu Gly Gln Glu Ile Thr Asp His Glu Ile Ala
 245 250 255
 Ser Leu Leu Tyr Ser Leu Leu Phe Ala Gly His Glu Thr Thr Thr Thr
 260 265 270
 Leu Ile Ser Asn Cys Phe Arg Val Leu Leu Asp His Pro Glu Gln Trp
 275 280 285
 Gln Ala Ile Leu Glu Asn Pro Lys Leu Ile Pro Ala Ala Val Asp Glu
 290 295 300
 Val Leu Arg Tyr Ser Gly Ser Ile Val Gly Trp Arg Arg Lys Ala Leu
 305 310 315 320
 Lys Asp Thr Glu Ile Gly Gly Val Ala Ile Lys Glu Gly Asp Gly Val
 325 330 335
 Leu Leu Leu Met Gly Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn
 340 345 350
 Gly Glu Glu Phe Asp Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser
 355 360 365
 Phe Gly Phe Gly Ile His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu
 370 375 380
 Gln Ala Lys Ile Cys Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu
 385 390 395 400
 His Leu Val Ala Asp Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe

405

410

415

Arg Val Pro Thr Ser Val Pro Val Thr Trp Asn Ala
420 425

<210> 781

<211> 978

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(955)

<223> RXN00387

<400> 781

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gatttctccg ccgactacct cgccaacggg ccaggccgag atg ttc cgc tcg aat 115
Met Phe Arg Ser Asn
1 5

att tcc tac gca gtc ggc gac gac atc caa aac gac cca gaa acc tgg 163
Ile Ser Tyr Ala Val Gly Asp Asp Ile Gln Asn Asp Pro Glu Thr Trp
10 15 20

gaa gac tac gaa ctt cgc gtc aac cac cca ctg cgc atc gaa ggc gac 211
Glu Asp Tyr Glu Leu Arg Val Asn His Pro Leu Arg Ile Glu Gly Asp
25 30 35

cgc gtc tac ctt cag ggc cac ggc ttc gcc cca aca ttc acc gtg acc 259
Arg Val Tyr Leu Gln Gly His Gly Phe Ala Pro Thr Phe Thr Val Thr
40 45 50

tgg cca aat ggc gag acc cgc acc cag acc gtg cag tgg cgc cca gac 307
Trp Pro Asn Gly Glu Thr Arg Thr Gln Thr Val Gln Trp Arg Pro Asp
55 60 65

gac ccg acc ttc ttc ctg tcc tca ggc gtg gtc cgt ttc gat cca ccc 355
Asp Pro Thr Phe Phe Leu Ser Ser Gly Val Val Arg Phe Asp Pro Pro
70 75 80 85

gcc ggc atg tac cca gac ctt tac gag cgc cgc caa aac cag ttg gcc 403
Ala Gly Met Tyr Pro Asp Leu Tyr Glu Arg Arg Gln Asn Gln Leu Ala
90 95 100

atc cag gga ctt ttc gca ccg acc gcg gaa tgg gaa ggc gac aac aac 451
Ile Gln Gly Leu Phe Ala Pro Thr Ala Glu Trp Glu Gly Asp Asn Asn
105 110 115

gaa ctg ctg acc tcc tcc tac ccg gcg atg cgt gac cca gcc gtg gcg 499
Glu Leu Leu Thr Ser Ser Tyr Pro Ala Met Arg Asp Pro Ala Val Ala
120 125 130

atc gat att tac cgc ggc gac aat ggc ctc gat acc ggc atc gga cag 547
Ile Asp Ile Tyr Arg Gly Asp Asn Gly Leu Asp Thr Gly Ile Gly Gln
135 140 145

tca ttg ttc agc ctg gac tct agt ctc atg cac agc ggc gtg ctg caa 595
Ser Leu Phe Ser Leu Asp Ser Ser Leu Met His Ser Gly Val Leu Gln

150	155	160	165	
aaa att gag cgc gtc aac ctc caa atc ggc gac acc gtc acc ctg gat				643
Lys Ile Glu Arg Val Asn Leu Gln Ile Gly Asp Thr Val Thr Leu Asp				
	170	175	180	
gat ggc acc acc gtc tcc ttc gac ggc gcg tca gaa ttt gcc aac tac				691
Asp Gly Thr Thr Val Ser Phe Asp Gly Ala Ser Glu Phe Ala Asn Tyr				
	185	190	195	
cag atc agc cgc gac ccc aca caa aac tgg gtg ctg gtc acc acc gtg				739
Gln Ile Ser Arg Asp Pro Thr Gln Asn Trp Val Leu Val Thr Thr Val				
	200	205	210	
att tgc ctg gtc tcc ctg gtt gga tcc ctg atg atc cga cgc cgc cgc				787
Ile Ser Leu Val Ser Leu Val Gly Ser Leu Met Ile Arg Arg Arg Arg				
	215	220	225	
att tgg gtg cgt ttc tat cca caa gaa aac gga acc acc cgc gtg gaa				835
Ile Trp Val Arg Phe Tyr Pro Gln Glu Asn Gly Thr Thr Arg Val Glu				
	230	235	240	245
acc ggc gga ctt gcc cgc acc gac cgc gca ggc tgg ggt ggc gaa tac				883
Thr Gly Gly Leu Ala Arg Thr Asp Arg Ala Gly Trp Gly Gly Glu Tyr				
	250	255	260	
gag aaa ttc cac cgc gaa ctg ctg ggt ctg aag gag gaa gat gaa gac				931
Glu Lys Phe His Arg Glu Leu Leu Gly Leu Lys Glu Glu Asp Glu Asp				
	265	270	275	
gaa gag tac ttc gac cac gac gac taacaccgca atttaaaggc ttt				978
Glu Glu Tyr Phe Asp His Asp Asp				
	280	285		

<210> 782

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 782

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	20	25	30
Arg Ile Glu Gly Asp Arg Val Tyr Leu Gln Gly His Gly Phe Ala Pro			
	35	40	45
Thr Phe Thr Val Thr Trp Pro Asn Gly Glu Thr Arg Thr Gln Thr Val			
	50	55	60
Gln Trp Arg Pro Asp Asp Pro Thr Phe Phe Leu Ser Ser Gly Val Val			
	65	70	75
Arg Phe Asp Pro Pro Ala Gly Met Tyr Pro Asp Leu Tyr Glu Arg Arg			
	85	90	95
Gln Asn Gln Leu Ala Ile Gln Gly Leu Phe Ala Pro Thr Ala Glu Trp			
	100	105	110

Glu Gly Asp Asn Asn Glu Leu Leu Thr Ser Ser Tyr Pro Ala Met Arg
 115 120 125
 Asp Pro Ala Val Ala Ile Asp Ile Tyr Arg Gly Asp Asn Gly Leu Asp
 130 135 140
 Thr Gly Ile Gly Gln Ser Leu Phe Ser Leu Asp Ser Ser Leu Met His
 145 150 155 160
 Ser Gly Val Leu Gln Lys Ile Glu Arg Val Asn Leu Gln Ile Gly Asp
 165 170 175
 Thr Val Thr Leu Asp Asp Gly Thr Thr Val Ser Phe Asp Gly Ala Ser
 180 185 190
 Glu Phe Ala Asn Tyr Gln Ile Ser Arg Asp Pro Thr Gln Asn Trp Val
 195 200 205
 Leu Val Thr Thr Val Ile Ser Leu Val Ser Leu Val Gly Ser Leu Met
 210 215 220
 Ile Arg Arg Arg Arg Ile Trp Val Arg Phe Tyr Pro Gln Glu Asn Gly
 225 230 235 240
 Thr Thr Arg Val Glu Thr Gly Gly Leu Ala Arg Thr Asp Arg Ala Gly
 245 250 255
 Trp Gly Gly Glu Tyr Glu Lys Phe His Arg Glu Leu Leu Gly Leu Lys
 260 265 270
 Glu Glu Asp Glu Asp Glu Glu Tyr Phe Asp His Asp Asp
 275 280 285

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(54) Title: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISM
AND ENERGY PRODUCTION(57) Abstract: Isolated nucleic acid molecules, designated SMP nucleic acid molecules, which encode novel SMP proteins from
Corynebacterium glutamicum are described. The invention also provides antisense nucleic acid molecules, recombinant expression
vectors containing SMP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention
still further provides isolated SMP proteins, mutated SMP proteins, fusion proteins, antigenic peptides and methods for the improve-
ment of production of a desired compound from *C. glutamicum* based on genetic engineering of SMP genes in this organism.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 00/00943

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/31 C12N15/55 C12N1/21 C12N9/18 C07K14/34
 C12P13/08 C12Q1/68 //(C12N15/55,C12R1:15)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K C12P C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	PETERS-WENDISCH ET AL: "Pyruvate carboxylase as an anaplerotic enzyme in <i>Corynebacterium glutamicum</i> " MICROBIOLOGY, SOCIETY FOR GENERAL MICROBIOLOGY, READING, GB, vol. 143, no. PART 04, April 1997 (1997-04), pages 1095-1103, XP002110209 ISSN: 1350-0872 the whole document ---	1-3, 8-19, 22-34
X	EIKMANN ET AL: "The phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : molecular cloning, nucleotide sequence, and expression" MOL. GEN. GENET., vol. 218, 1989, pages 330-339, XP002138580 the whole document ---	1-3, 8-19, 22-34
	--- -/--	

☒ Further documents are listed in the continuation of box C.☐ Patent family members are listed in annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

2 November 2000

Date of mailing of the international search report

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Galli, I

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 00/00943

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL SEQUENCES [Online] Accession No. 006814, 1 November 1997 (1997-11-01) COLE S.T.: "6-phosphogluconolactolase (6PGL) of Mycobacterium tuberculosis" XP002151659 52% identity at the amino acid level (Seq. 2) and 60% at nucleotide level (seq. 1). & COLE S.T. ET AL.: "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence" NATURE, vol. 393, 1998, pages 537-544, XP002151645 ---	6-17,37, 38
A	BATHE B. ET AL.: "A physical and genetic map of the Corynebacterium glutamicum ATCC13032 chromosome" MOL. GEN. GENET., vol. 252, 1996, pages 255-265, XP002151646 the whole document, in particular table 3. -----	1-38

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 00/00943

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see subject 1. on extra sheet

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-38, partly

An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an SMP protein or a portion thereof, said nucleic acid being characterized by seq. ID 1. An isolated nucleic acid comprising a nucleotide sequence at least 50% homologous to seq. 1. Corresponding polypeptides (seq. 2.). Corresponding vectors, recombinant host cells, production methods. Use in diagnosis of *C. diphtheriae*.

2-293. Claims 1-38, partly

Idem as subject-matter 1, but limited to the pairs of sequences listed in Table 1 (except those disclaimed).